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## SEQUENCE LISTING

TECH CENTER 1600/2900

&lt;110&gt; MIYATA, Toshio

<120> A Method for Detecting Megsin Protein and Use  
Thereof

&lt;130&gt; SHIM-012

&lt;140&gt; 09/936,883

&lt;141&gt; 2001-12-21

&lt;150&gt; JP 1999-75305

&lt;151&gt; 1999-03-19

&lt;150&gt; JP 1999-306623

&lt;151&gt; 1999-10-28

&lt;160&gt; 21

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1140)

&lt;300&gt;

<302> A mesangium-predominant gene, megsin, is a new serpin  
upregulated in IgA nephropathy.

&lt;303&gt; J. Clin. Invest.

&lt;304&gt; 120

&lt;305&gt; 4

&lt;306&gt; 828-836

&lt;307&gt; 1998-08-15

&lt;400&gt; 1

atg gcc tcc ctt gct gca gca aat gca gag ttt tgc ttc aac ctg ttc 48  
Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe  
1 5 10 15

aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct 96  
Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser  
20 25 30

ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat 144  
Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp  
35 40 45

gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca 192  
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser  
50 55 60

gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg 240  
 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu  
 65 70 75 80  
 aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc 288  
 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu  
 85 90 95  
 agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag 336  
 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys  
 100 105 110  
 gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga 384  
 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg  
 115 120 125  
 gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag 432  
 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys  
 130 135 140  
 tgg gtt gaa aat gaa aca cat ggc aaa atc aag aac gtg att ggt gaa 480  
 Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu  
 145 150 155 160  
 ggt ggc ata agc tca tct gct gta atg gtg ctg gtg aat gct gtg tac 528  
 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
 165 170 175  
 ttc aaa ggc aag tgg caa tca gcc ttc acc aag agc gaa acc ata aat 576  
 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn  
 180 185 190  
 tgc cat ttc aaa tct ccc aag tgc tct ggg aag gca gtc gcc atg atg 624  
 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met  
 195 200 205  
 cat cag gaa cgg aag ttc aat ttg tct gtt att gag gac cca tca atg 672  
 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met  
 210 215 220  
 aag att ctt gag ctc aga tac aat ggt ggc ata aac atg tac gtt ctg 720  
 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu  
 225 230 235 240  
 ctg cct gag aat gac ctc tct gaa att gaa aac aaa ctg acc ttt cag 768  
 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln  
 245 250 255  
 aat cta atg gaa tgg acc aat cca agg cga atg acc tct aag tat gtt 816  
 Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val  
 260 265 270  
 gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa 864  
 Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys  
 275 280 285  
 caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa 912

Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys  
 290 295 300  
 gca gat ctc tct ggg att gct tcg ggg ggt cgt ctg tat ata tca agg 960  
 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg  
 305 310 315 320  
 atg atg cac aaa tct tac ata gag gtc act gag gag ggc acc gag gct 1008  
 Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala  
 325 330 335  
 act gct gcc aca gga agt aat att gta gaa aag caa ctc cct cag tcc 1056  
 Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser  
 340 345 350  
 acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat 1104  
 Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp  
 355 360 365  
 gac atc atc tta ttc agt ggc aaa gtt tct tgc cct tga 1143  
 Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro  
 370 375 380

<210> 2  
 <211> 380  
 <212> PRT  
 <213> Homo sapiens

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 Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp  
 35 40 45  
 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser  
 50 55 60  
 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu  
 65 70 75 80  
 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu  
 85 90 95  
 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys  
 100 105 110  
 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg  
 115 120 125  
 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys  
 130 135 140

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu  
 145 150 155 160  
 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
 165 170 175  
 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn  
 180 185 190  
 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met  
 195 200 205  
 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met  
 210 215 220  
 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu  
 225 230 235 240  
 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln  
 245 250 255  
 Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val  
 260 265 270  
 Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys  
 275 280 285  
 Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys  
 290 295 300  
 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg  
 305 310 315 320  
 Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala  
 325 330 335  
 Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser  
 340 345 350  
 Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp  
 355 360 365  
 Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro  
 370 375 380

<210> 3  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Artificially  
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<220>  
 <221> misc\_feature

<222> 26, 29

<223> n is a or g or c or t.

<400> 3

gtgaatgctg tgtacttaaa ggcaantgn

29

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized degenerative primer sequence

<220>

<221> misc\_feature

<222> 3, 9, 15

<223> n is a or g or c or t.

<400> 4

aanagraang grtcngc

17

<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized degenerative primer sequence

<220>

<221> misc\_feature

<222> 6, 9, 12, 15, 18, 21

<223> n is a or g or c or t.

<400> 5

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26

<210> 6

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized degenerative primer sequence

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cgacctccag aggcaattcc agagagatca gccctgg

37

<210> 7

<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
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<210> 8  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized antisense primer sequence

<400> 8  
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<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
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<400> 9  
ctgacgtgca cagtcacctc gagcacc 27

<210> 10  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
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<400> 10  
gaggtctcag aagaaggcac tgaggcaact gctgcc 36

<210> 11  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 11

Phe Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe  
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<210> 12

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 12

Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val Phe Ser Asp  
1 5 10 15

<210> 13

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 13

Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu  
1 5 10 15

<210> 14

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 14

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val  
1 5 10 15

<210> 15

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 15  
 Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu Phe Arg  
 1 5 10 15

<210> 16  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Artificially  
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<400> 16  
 Leu Gly Leu Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp  
 1 5 10

<210> 17  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Artificially  
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<400> 17  
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<210> 18  
 <211> 1229  
 <212> DNA  
 <213> Rattus norvegicus

<220>  
 <221> CDS  
 <222> (8)..(1147)

<220>  
 <221> misc\_feature  
 <222> 158, 159, 160, 287, 288, 289  
 <223> n is a or g or c or t.

<300>  
 <310> PCT/JP98/04269  
 <311> 1998-09-22

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 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp  
 1 5 10

tta ttc aga gag atg gat agt agt caa gga aac gga aat gta ttc ttc 97



Leu	Phe	Arg	Glu	Met	Asp	Ser	Ser	Gln	Gly	Asn	Gly	Asn	Val	Phe	Phe	
15					20					25					30	
tct	tcc	ctg	agc	atc	ttc	act	gcc	ctg	agc	cta	atc	cgt	ttg	ggg	gct	145
Ser	Ser	Leu	Ser	Ile	Phe	Thr	Ala	Leu	Ser	Leu	Ile	Arg	Leu	Gly	Ala	
				35					40					45		
cga	ggg	gac	tgt	nnn	cgt	cag	att	gac	aag	gcc	ctg	cac	ttt	atc	tcc	193
Arg	Gly	Asp	Cys	Xaa	Arg	Gln	Ile	Asp	Lys	Ala	Leu	His	Phe	Ile	Ser	
			50					55					60			
cca	tca	aga	caa	ggg	aat	tca	tcg	aac	agt	cag	cta	gga	ctg	caa	tat	241
Pro	Ser	Arg	Gln	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Leu	Gly	Leu	Gln	Tyr	
		65					70					75				
caa	ttg	aaa	aga	gtt	ctt	gct	gac	ata	aac	tca	tct	cat	aag	gat	nnn	289
Gln	Leu	Lys	Arg	Val	Leu	Ala	Asp	Ile	Asn	Ser	Ser	His	Lys	Asp	Xaa	
	80					85					90					
aaa	ctc	agc	att	gcc	aat	gga	gtt	ttt	gca	gag	aaa	gta	ttt	gat	ttt	337
Lys	Leu	Ser	Ile	Ala	Asn	Gly	Val	Phe	Ala	Glu	Lys	Val	Phe	Asp	Phe	
	95				100					105					110	
cat	aag	agc	tat	atg	gag	tgt	gct	gaa	aac	tta	tac	aat	gct	aaa	gtg	385
His	Lys	Ser	Tyr	Met	Glu	Cys	Ala	Glu	Asn	Leu	Tyr	Asn	Ala	Lys	Val	
				115					120					125		
gaa	aga	gtt	gat	ttt	aca	aat	gat	ata	caa	gaa	acc	aga	ttt	aaa	att	433
Glu	Arg	Val	Asp	Phe	Thr	Asn	Asp	Ile	Gln	Glu	Thr	Arg	Phe	Lys	Ile	
			130					135					140			
aat	aaa	tgg	att	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aag	gtg	ttg	481
Asn	Lys	Trp	Ile	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Lys	Val	Leu	
		145					150					155				
ggg	gac	agc	agc	ctc	agc	tca	tca	gct	gtc	atg	gtg	cta	gtg	aat	got	529
Gly	Asp	Ser	Ser	Leu	Ser	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala	
	160					165					170					
gtt	tac	ttc	aaa	ggc	aag	tgg	aaa	tcg	gcc	ttc	acc	aag	agt	gat	acc	577
Val	Tyr	Phe	Lys	Gly	Lys	Trp	Lys	Ser	Ala	Phe	Thr	Lys	Ser	Asp	Thr	
	175				180					185					190	
ctc	agt	tgc	cat	ttc	agg	tct	ccc	agc	ggg	cct	gga	aaa	gca	gtt	aat	625
Leu	Ser	Cys	His	Phe	Arg	Ser	Pro	Ser	Gly	Pro	Gly	Lys	Ala	Val	Asn	
				195					200					205		
atg	atg	cat	caa	gaa	cgg	agg	ttc	aat	ttg	tct	acc	att	cag	gag	cca	673
Met	Met	His	Gln	Glu	Arg	Arg	Phe	Asn	Leu	Ser	Thr	Ile	Gln	Glu	Pro	
			210					215					220			
cca	atg	cag	att	ctt	gag	cta	caa	tat	cat	ggg	ggc	ata	agc	atg	tac	721
Pro	Met	Gln	Ile	Leu	Glu	Leu	Gln	Tyr	His	Gly	Gly	Ile	Ser	Met	Tyr	
		225					230					235				
atc	atg	ttg	ccc	gag	gat	gac	cta	tcc	gaa	att	gaa	agc	aag	ctg	agt	769
Ile	Met	Leu	Pro	Glu	Asp	Asp	Leu	Ser	Glu	Ile	Glu	Ser	Lys	Leu	Ser	

240	245	250	
ttc cag aat cta atg gac tgg aca aat agc agg aag atg aaa tct cag			817
Phe Gln Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln			
255	260	265	270
tat gtg aat gtg ttt ctc ccc cag ttc aag ata gag aaa gat tat gaa			865
Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu			
	275	280	285
atg agg agc cac ttg aaa tct gta ggc ttg gaa gac atc ttt gtt gag			913
Met Arg Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu			
	290	295	300
tcc agg gct gat ctg tct gga att gcc tct gga ggt cgt ctc tat gta			961
Ser Arg Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val			
	305	310	315
tca aag cta atg cac aag tcc ctc ata gag gtc tca gaa gaa ggc acc			1009
Ser Lys Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr			
	320	325	330
gag gca act gct gcc aca gaa agt aac atc gtt gaa aag cta ctt cct			1057
Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro			
	335	340	345
gaa tcc acg gtg ttc aga gct gac cgc ccc ttt ctg ttt gtc att agg			1105
Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg			
	355	360	365
aag aat ggc atc atc tta ttt act ggc aaa gtc tcg tgt cct			1147
Lys Asn Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro			
	370	375	380
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aattgtaatt ggaagtacat gg			1229

<210> 19  
 <211> 380  
 <212> PRT  
 <213> Rattus norvegicus

<220>  
 <221> misc\_feature  
 <222> 51, 94  
 <223> Xaa is unknown.

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Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly

35

40

45

~~Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser  
50 55 60  
Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu  
65 70 75 80  
Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu  
85 90 95  
Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys  
100 105 110  
Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg  
115 120 125  
Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys  
130 135 140  
Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp  
145 150 155 160  
Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
165 170 175  
Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser  
180 185 190  
Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met  
195 200 205  
His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met  
210 215 220  
Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met  
225 230 235 240  
Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln  
245 250 255  
Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val  
260 265 270  
Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg  
275 280 285  
Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg  
290 295 300  
Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys  
305 310 315 320  
Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala  
325 330 335  
Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser~~

340

345

350

Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn  
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Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro  
 370 375 380

<210> 20  
 <211> 1147  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(1104)

<300>  
 <310> PCT/JP98/04269  
 <311> 1998-09-22

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 ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg 96  
 Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu  
 20 25 30  
 ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt 144  
 Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe  
 35 40 45  
 aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt 192  
 Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu  
 50 55 60  
 cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag 240  
 Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys  
 65 70 75 80  
 gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat 288  
 Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr  
 85 90 95  
 gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct 336  
 Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala  
 100 105 110  
 aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt 384  
 Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe  
 115 120 125  
 aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag 432  
 Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys

130	135	140	
gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg			480
Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val			
145	150	155	160
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act			528
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr			
	165	170	175
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta			576
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val			
	180	185	190
gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag			624
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln			
	195	200	205
cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc			672
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser			
	210	215	220
atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag			720
Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys			
	225	230	235
ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa			768
Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys			
	245	250	255
tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat			816
Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn			
	260	265	270
tat gaa atg acg cac cac ttg aaa tcc tta ggc ttg aaa gat atc ttt			864
Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe			
	275	280	285
gat gag tcc agt gca gat ctc tct gga att gcc tct gga ggt cgt ctc			912
Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu			
	290	295	300
tac gta tca aag cta atg cac aag tca ttc ata gag gtc tca gag gag			960
Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu			
	305	310	315
ggc act gaa gcc act gct gcc aca gaa aat aac att gtt gaa aag cag			1008
Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln			
	325	330	335
ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc			1056
Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val			
	340	345	350
atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct			1104
Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro			
	355	360	365

tgaaattcga ttgtgtttcc tatacagtaa caggcatcaa gaa

1147

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<400> 21

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Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu  
20 25 30

Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe  
35 40 45

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu  
50 55 60

Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys  
65 70 75 80

Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr  
85 90 95

Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala  
100 105 110

Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe  
115 120 125

Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys  
130 135 140

Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val  
145 150 155 160

Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr  
165 170 175

Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val  
180 185 190

Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln  
195 200 205

Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser  
210 215 220

Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys  
225 230 235 240

Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys  
245 250 255

Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn  
260 265 270

Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe  
275 280 285

Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu  
290 295 300

Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu  
305 310 315 320

Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln  
325 330 335

Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val  
340 345 350

Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro  
355 360 365

B1  
cancel  
C1